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RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/029,756

DATE: 01/18/2002

TIME: 09:18:30

Input Set : N:\Crf3\RULE60\10029756.raw

Output Set: N:\CRF3\01182002\J029756.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Thomas, Terry L.

8 (ii) TITLE OF INVENTION: PRODUCTION OF GAMMA LINOLENIC ACID BY A
9 DELTA 6-DESATURASE

11 (iii) NUMBER OF SEQUENCES: 27

13 (iv) CORRESPONDENCE ADDRESS:

15 (A) ADDRESSEE: Scully, Scott, Murphy & Presser

16 (B) STREET: 400 Garden City Plaza

17 (C) CITY: Garden City

18 (D) STATE: New York

19 (E) COUNTRY: United States

20 (F) ZIP: 11530

22 (v) COMPUTER READABLE FORM:

24 (A) MEDIUM TYPE: Floppy disk

25 (B) COMPUTER: IBM PC compatible

26 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

27 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

29 (vi) CURRENT APPLICATION DATA:

C--> 31 (A) APPLICATION NUMBER: US/10/029,756

C--> 32 (B) FILING DATE: 21-Dec-2001

33 (C) CLASSIFICATION:

35 (vii) PRIOR APPLICATION DATA:

37 (A) APPLICATION NUMBER: 08/934,254

38 (B) FILING DATE:

42 (viii) ATTORNEY/AGENT INFORMATION:

44 (A) NAME: Presser, Leopold

45 (B) REGISTRATION NUMBER: 19,827

46 (C) REFERENCE/DOCKET NUMBER: 8383ZYXWVU

48 (ix) TELECOMMUNICATION INFORMATION:

49 (A) TELEPHONE: (516) 742-4343

50 (B) TELEFAX: (516) 742-4366

51 (C) TELEX: 230 901 SANS UR

53 (2) INFORMATION FOR SEQ ID NO: 1:

55 (i) SEQUENCE CHARACTERISTICS:

57 (A) LENGTH: 3588 base pairs

58 (B) TYPE: nucleic acid

59 (C) STRANDEDNESS: both

60 (D) TOPOLOGY: linear

62 (ii) MOLECULE TYPE: DNA (genomic)

64 (ix) FEATURE:

66 (A) NAME/KEY: CDS

67 (B) LOCATION: 2002..3081

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69      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
71      GCTAGCCACC AGTGACGATG CCTTGAATTT GGCCATTCTG ACCCAGGCCG GTATTCTGAA      60
73      TCCCCGCATT CGCATTGTTA ATCGTTTGTT CAACCATGCC CTGGGTAAAC GTTTAGACAC      120
75      CACCTTGCCA GACCACGTTA GTTTGAGTGT TTCCGCCCTG GCGGCCCCGA TTTTTCCTT      180
77      TGCGGCTTTG GGCAATCAGG CGATCGGGCA ATTGCGTTTG TTTGACCAGA CTGGGCCAT      240
79      TCAGGAAATT GTCATTCACC AAGACCATCC CTGGCTCAAT TTACCCCTGG CGGATTTATG      300
81      GGATGATCCG AGCCGAATGT TGATCTATTA CCTACCGGCC CACAGTGAAA CGGATTTAGT      360
83      AGGCGCAGTG GTGAATAATT TAACGTTGCA ATCTGGGGAC CATTTAATAG TGGGACAAAA      420
85      ACCCCAACCC AAGACCAAAC GCGATCGCC TTGGCGCAA TTTTCCAAAC TGATTACCAA      480
87      CCTGCGGGAG TATCAGCGGT ATGTCCAACA GGTGATATGG GTGGTGTGT TTTTATTGTT      540
89      GATGATTTTT CTGGCCACCT TCATCTACGT TTCCATTGAT CAACATATTG CCCCAGTGGG      600
91      CGCGTTGTAT TTTTCCGTGG GCATGATTAC CGGGGCCGGT GGCAAGGAAG AGGTGGCCGA      660
93      AAAGTCCCCC GATATCATCA AAGTATTCAC AGTGGTGATG ATGATCGCCG GGGCGGGGGT      720
95      GATTGGTATT TGTATGCCC TACTGAATGA TTTCATCCTT GGCAGTCGCT TTAGTCAGTT      780
97      TTTGGATGCG GCCAAGTTAC CCGATCGCCA TCACATCATC ATTTGTGGGC TGGGGGGAGT      840
99      GAGCATGGCC ATTATTGAAG AGTTAATCA CCAGGGCCAT GAAATTGTGG TAATCGAAAA      900
101     GGATACAGAT AATCGTTTCT TGCATACGGC CCGTCCCTG GGGGTGCCCC TAATTGTGGA      960
103     GGATGCCCCG CTAGAAAGAA CGTTGGCCTG CGCCAATATC AACCGAGCCG AAGCCATTGT      1020
105     GGTGGCCACC AGCGACGACA CCGTAACTT GGAAATTGGC CTAAGTCCCA AGGCGATCGC      1080
107     CCCTAGCCTG CCAGTGGTGT TGCGTTGCCA GGATGCCAG TTTAGCCTGT CCCTGCAGGA      1140
109     AGTATTTGAA TTTGAAACGG TGCTTTGTCC GGCGGAATTG GCCACCTATT CCTTTGCGGC      1200
111     GGCGGCCCTG GGGGGCAAAA TTTTGGGCAA CGGCATGACC GATGATTTGC TGTGGGTAGC      1260
113     CCTAGCCACC TTAATCACTC CTAACCATCC CTTTGGCGAC CAATTGGTTA AAATTGCAGC      1320
115     CCAAAAGTCT GATTTTCGTT CCCTCTATCT AGAACGGGGT GGCAAAACCA TCCATAGCTG      1380
117     GGAATTATTG GGTACCCATC TCGACTCTGG AGACGTGTTG TATTTAACCA TGCCCCGCCA      1440
119     TGCCCTAGAG CAACTTTGGC GATCGCCCCG TGCCACTGCT GATCCTCTGG ACTCTTTTTT      1500
121     GGTTTAGCAT GGGGGGATGG AACTCTTGAC TCGGCCCAAT GGTGATCAAG AAAGAACGCT      1560
123     TTGTCTATGT TTAGTATTTT TAAGTTAACC AACAGCAGAG GATAACTTCC AAAAGAAATT      1620
125     AAGCTCAAAA AGTAGCAAAA TAAGTTTAAT TCATAACTGA GTTTTACTGC TAAACAGCGG      1680
127     TGCAAAAAG TCAGATAAAA TAAAAGCTTC ACTTCGGTTT TATATTGTGA CCATGGTTCC      1740
129     CAGGCATCTG CTCTAGGGAG TTTTCCGCT GCCTTTAGAG AGTATTTTCT CCAAGTCGGC      1800
131     TAACTCCCCC ATTTTTCGCT AAAATCATAT ACAGACTATC CCAATATTGC CAGAGCTTTG      1860
133     ATGACTCACT GTAGAAGGCA GACTAAAATT CTAGCAATGG ACTCCAGTT GGAATAAATT      1920
135     TTTAGTCTCC CCCGCGCTG GAGTTTTTTT GTAGTTAATG GCGGTATAAT GTGAAAGTTT      1980
137     TTTATCTATT TAAATTTATA A ATG CTA ACA GCG GAA AGA ATT AAA TTT ACC      2031
138                                     Met Leu Thr Ala Glu Arg Ile Lys Phe Thr
139                                     1 5 10
141     CAG AAA CGG GGG TTT CGT CGG GTA CTA AAC CAA CGG GTG GAT GCC TAC      2079
142     Gln Lys Arg Gly Phe Arg Arg Val Leu Asn Gln Arg Val Asp Ala Tyr
143                                     15 20 25
145     TTT GCC GAG CAT GGC CTG ACC CAA AGG GAT AAT CCC TCC ATG TAT CTG      2127
146     Phe Ala Glu His Gly Leu Thr Gln Arg Asp Asn Pro Ser Met Tyr Leu
147                                     30 35 40
149     AAA ACC CTG ATT ATT GTG CTC TGG TTG TTT TCC GCT TGG GCC TTT GTG      2175
150     Lys Thr Leu Ile Ile Val Leu Trp Leu Phe Ser Ala Trp Ala Phe Val
151                                     45 50 55
153     CTT TTT GCT CCA GTT ATT TTT CCG GTG CGC CTA CTG GGT TGT ATG GTT      2223
154     Leu Phe Ala Pro Val Ile Phe Pro Val Arg Leu Leu Gly Cys Met Val
155     60 65 70

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157	TTG	GCG	ATC	GCC	TTG	GCG	GCC	TTT	TCC	TTC	AAT	GTC	GGC	CAC	GAT	GCC	2271
158	Leu	Ala	Ile	Ala	Leu	Ala	Phe	Ser	Phe	Asn	Val	Gly	His	Asp	Ala		
159	75					80					85				90		
161	AAC	CAC	AAT	GCC	TAT	TCC	TCC	AAT	CCC	CAC	ATC	AAC	CGG	GTT	CTG	GGC	2319
162	Asn	His	Asn	Ala	Tyr	Ser	Ser	Asn	Pro	His	Ile	Asn	Arg	Val	Leu	Gly	
163					95					100					105		
165	ATG	ACC	TAC	GAT	TTT	GTC	GGG	TTA	TCT	AGT	TTT	CTT	TGG	CGC	TAT	CGC	2367
166	Met	Thr	Tyr	Asp	Phe	Val	Gly	Leu	Ser	Ser	Phe	Leu	Trp	Arg	Tyr	Arg	
167					110					115				120			
169	CAC	AAC	TAT	TTG	CAC	CAC	ACC	TAC	ACC	AAT	ATT	CTT	GGC	CAT	GAC	GTG	2415
170	His	Asn	Tyr	Leu	His	His	Thr	Tyr	Thr	Asn	Ile	Leu	Gly	His	Asp	Val	
171			125						130					135			
173	GAA	ATC	CAT	GGA	GAT	GGC	GCA	GTA	CGT	ATG	AGT	CCT	GAA	CAA	GAA	CAT	2463
174	Glu	Ile	His	Gly	Asp	Gly	Ala	Val	Arg	Met	Ser	Pro	Glu	Gln	Glu	His	
175		140					145					150					
177	GTT	GGT	ATT	TAT	CGT	TTC	CAG	CAA	TTT	TAT	ATT	TGG	GGT	TTA	TAT	CTT	2511
178	Val	Gly	Ile	Tyr	Arg	Phe	Gln	Gln	Phe	Tyr	Ile	Trp	Gly	Leu	Tyr	Leu	
179	155					160					165					170	
181	TTC	ATT	CCC	TTT	TAT	TGG	TTT	CTC	TAC	GAT	GTC	TAC	CTA	GTG	CTT	AAT	2559
182	Phe	Ile	Pro	Phe	Tyr	Trp	Phe	Leu	Tyr	Asp	Val	Tyr	Leu	Val	Leu	Asn	
183					175					180					185		
185	AAA	GGC	AAA	TAT	CAC	GAC	CAT	AAA	ATT	CCT	CCT	TTC	CAG	CCC	CTA	GAA	2607
186	Lys	Gly	Lys	Tyr	His	Asp	His	Lys	Ile	Pro	Pro	Phe	Gln	Pro	Leu	Glu	
187					190					195				200			
189	TTA	GCT	AGT	TTG	CTA	GGG	ATT	AAG	CTA	TTA	TGG	CTC	GGC	TAC	GTT	TTC	2655
190	Leu	Ala	Ser	Leu	Leu	Gly	Ile	Lys	Leu	Leu	Trp	Leu	Gly	Tyr	Val	Phe	
191			205					210					215				
193	GGC	TTA	CCT	CTG	GCT	CTG	GGC	TTT	TCC	ATT	CCT	GAA	GTA	TTA	ATT	GGT	2703
194	Gly	Leu	Pro	Leu	Ala	Leu	Gly	Phe	Ser	Ile	Pro	Glu	Val	Leu	Ile	Gly	
195		220					225					230					
197	GCT	TCG	GTA	ACC	TAT	ATG	ACC	TAT	GGC	ATC	GTG	GTT	TGC	ACC	ATC	TTT	2751
198	Ala	Ser	Val	Thr	Tyr	Met	Thr	Tyr	Gly	Ile	Val	Val	Cys	Thr	Ile	Phe	
199	235					240					245					250	
201	ATG	CTG	GCC	CAT	GTG	TTG	GAA	TCA	ACT	GAA	TTT	CTC	ACC	CCC	GAT	GGT	2799
202	Met	Leu	Ala	His	Val	Leu	Glu	Ser	Thr	Glu	Phe	Leu	Thr	Pro	Asp	Gly	
203					255					260					265		
205	GAA	TCC	GGT	GCC	ATT	GAT	GAC	GAG	TGG	GCT	ATT	TGC	CAA	ATT	CGT	ACC	2847
206	Glu	Ser	Gly	Ala	Ile	Asp	Asp	Glu	Trp	Ala	Ile	Cys	Gln	Ile	Arg	Thr	
207				270					275					280			
209	ACG	GCC	AAT	TTT	GCC	ACC	AAT	AAT	CCC	TTT	TGG	AAC	TGG	TTT	TGT	GGC	2895
210	Thr	Ala	Asn	Phe	Ala	Thr	Asn	Asn	Pro	Phe	Trp	Asn	Trp	Phe	Cys	Gly	
211			285					290						295			
213	GGT	TTA	AAT	CAC	CAA	GTT	ACC	CAC	CAT	CTT	TTC	CCC	AAT	ATT	TGT	CAT	2943
214	Gly	Leu	Asn	His	Gln	Val	Thr	His	His	Leu	Phe	Pro	Asn	Ile	Cys	His	
215		300					305					310					
217	ATT	CAC	TAT	CCC	CAA	TTG	GAA	AAT	ATT	ATT	AAG	GAT	GTT	TGC	CAA	GAG	2991
218	Ile	His	Tyr	Pro	Gln	Leu	Glu	Asn	Ile	Ile	Lys	Asp	Val	Cys	Gln	Glu	
219	315					320					325					330	
221	TTT	GGT	GTG	GAA	TAT	AAA	GTT	TAT	CCC	ACC	TTC	AAA	GCG	GCG	ATC	GCC	3039

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222 Phe Gly Val Glu Tyr Lys Val Tyr Pro Thr Phe Lys Ala Ala Ile Ala
223 335 340 345
225 TCT AAC TAT CGC TGG CTA GAG GCC ATG GGC AAA GCA TCG TGACATTGCC 3088
226 Ser Asn Tyr Arg Trp Leu Glu Ala Met Gly Lys Ala Ser
227 350 355
229 TTGGGATTGA AGCAAAATGG CAAAATCCCT CGTAAATCTA TGATCGAAGC CTTTCTGTTG 3148
231 CCCGCCGACC AAATCCCCGA TGCTGACCAA AGGTTGATGT TGGCATTGCT CCAAACCCAC 3208
233 TTTGAGGGGG TTCATTGGCC GCAGTTTCAA GCTGACCTAG GAGGCAAAGA TTGGGTGATT 3268
235 TTGCTCAAAT CCGCTGGGAT ATTGAAAGGC TTCACCACCT TTGGTTTCTA CCCTGCTCAA 3328
237 TGGGAAGGAC AAACCGTCAG AATTGTTTAT TCTGGTGACA CCATCACCGA CCCATCCATG 3388
239 TGGTCTAACC CAGCCCTGGC CAAGGCTTGG ACCAAGGCCA TGCAAATTCT CCACGAGGCT 3448
241 AGGCCAGAAA AATTATATTG GTCCTGATT TCTTCCGGCT ATCGCACCTA CCGATTTTGT 3508
243 AGCATTTTTG CCAAGGAATT CTATCCCCAC TATCTCCATC CCACTCCCCC GCCTGTACAA 3568
245 AATTTTATCC ATCAGCTAGC 3588
248 (2) INFORMATION FOR SEQ ID NO: 2:
250 (i) SEQUENCE CHARACTERISTICS:
252 (A) LENGTH: 359 amino acids
253 (B) TYPE: amino acid
254 (D) TOPOLOGY: linear
256 (ii) MOLECULE TYPE: protein
258 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
260 Met Leu Thr Ala Glu Arg Ile Lys Phe Thr Gln Lys Arg Gly Phe Arg
261 1 5 10 15
263 Arg Val Leu Asn Gln Arg Val Asp Ala Tyr Phe Ala Glu His Gly Leu
264 20 25 30
266 Thr Gln Arg Asp Asn Pro Ser Met Tyr Leu Lys Thr Leu Ile Ile Val
267 35 40 45
269 Leu Trp Leu Phe Ser Ala Trp Ala Phe Val Leu Phe Ala Pro Val Ile
270 50 55 60
272 Phe Pro Val Arg Leu Leu Gly Cys Met Val Leu Ala Ile Ala Leu Ala
273 65 70 75 80
275 Ala Phe Ser Phe Asn Val Gly His Asp Ala Asn His Asn Ala Tyr Ser
276 85 90 95
278 Ser Asn Pro His Ile Asn Arg Val Leu Gly Met Thr Tyr Asp Phe Val
279 100 105 110
281 Gly Leu Ser Ser Phe Leu Trp Arg Tyr Arg His Asn Tyr Leu His His
282 115 120 125
284 Thr Tyr Thr Asn Ile Leu Gly His Asp Val Glu Ile His Gly Asp Gly
285 130 135 140
287 Ala Val Arg Met Ser Pro Glu Gln Glu His Val Gly Ile Tyr Arg Phe
288 145 150 155 160
290 Gln Gln Phe Tyr Ile Trp Gly Leu Tyr Leu Phe Ile Pro Phe Tyr Trp
291 165 170 175
293 Phe Leu Tyr Asp Val Tyr Leu Val Leu Asn Lys Gly Lys Tyr His Asp
294 180 185 190
296 His Lys Ile Pro Pro Phe Gln Pro Leu Glu Leu Ala Ser Leu Leu Gly
297 195 200 205
299 Ile Lys Leu Leu Trp Leu Gly Tyr Val Phe Gly Leu Pro Leu Ala Leu
300 210 215 220

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302 Gly Phe Ser Ile Pro Glu Val Leu Ile Gly Ala Ser Val Thr Tyr Met
303 225 230 235 240
305 Thr Tyr Gly Ile Val Val Cys Thr Ile Phe Met Leu Ala His Val Leu
306 245 250 255
308 Glu Ser Thr Glu Phe Leu Thr Pro Asp Gly Glu Ser Gly Ala Ile Asp
309 260 265 270
311 Asp Glu Trp Ala Ile Cys Gln Ile Arg Thr Thr Ala Asn Phe Ala Thr
312 275 280 285
314 Asn Asn Pro Phe Trp Asn Trp Phe Cys Gly Gly Leu Asn His Gln Val
315 290 295 300
317 Thr His His Leu Phe Pro Asn Ile Cys His Ile His Tyr Pro Gln Leu
318 305 310 315 320
320 Glu Asn Ile Ile Lys Asp Val Cys Gln Glu Phe Gly Val Glu Tyr Lys
321 325 330 335
323 Val Tyr Pro Thr Phe Lys Ala Ala Ile Ala Ser Asn Tyr Arg Trp Leu
324 340 345 350
326 Glu Ala Met Gly Lys Ala Ser
327 355
330 (2) INFORMATION FOR SEQ ID NO: 3:
332 (i) SEQUENCE CHARACTERISTICS:
334 (A) LENGTH: 1884 base pairs
335 (B) TYPE: nucleic acid
336 (C) STRANDEDNESS: both
337 (D) TOPOLOGY: linear
339 (ii) MOLECULE TYPE: DNA (genomic)
341 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
343 AGCTTCACTT CGTTTTATA TTGTGACCAT GGTTCCCAGG CATCTGCTCT AGGGAGTTTT 60
345 TCCGCTGCCT TTAGAGAGTA TTTTCTCCAA GTCGGCTAAC TCCCCATTT TTAGGCAGAAA 120
347 TCATATACAG ACTATCCCAA TATTGCCAGA GCTTTGATGA CTCACTGTAG AAGGCAGACT 180
349 AAAATTCTAG CAATGGACTC CCAGTTGGAA TAAATTTTTA GTCTCCCCCG GCGCTGGAGT 240
351 TTTTTTGTAG TTAATGGCGG TATAATGTGA AAGTTTTTTA TCTATTTAAA TTTATAAATG 300
353 CTAACAGCGG AAAGAATTAA ATTTACCCAG AAACGGGGGT TTCGTCGGGT ACTAAACCAA 360
355 CGGGTGGATG CCTACTTTGC CGAGCATGGC CTGACCCAAA GGGATAATCC CTCCATGTAT 420
357 CTGAAAACCC TGATTATTGT GCTCTGGTTG TTTTCCGCTT GGGCCTTTGT GCTTTTTGCT 480
359 CCAGTTATTT TTCCGGTGCG CCTACTGGGT TGTATGGTTT TGGCGATCGC CTTGGCGGCC 540
361 TTTTCCTTCA ATGTCGGCCA CGATGCCAAC CACAATGCCT ATTCTTCCAA TCCCCACATC 600
363 AACCAGGTTT TGGGCATGAC CTACGATTTT GTCGGGTTAT CTAGTTTTCT TTGGCGCTAT 660
365 CGCCACAACCT ATTTGCACCA CACCTACACC AATATTCTTG GCCATGACGT GGAAATCCAT 720
367 GGAGATGGCG CAGTACGTAT GAGTCCTGAA CAAGAACATG TTGGTATTTA TCGTTTCCAG 780
369 CAATTTTATA TTTGGGGTTT ATATCTTTT ATTCCCTTTT ATTGGTTTCT CTACGATGTC 840
371 TACCTAGTGC TTAATAAAGG CAAATATCAC GACCATAAAA TTCCTCCTTT CCAGCCCCTA 900
373 GAATTAGCTA GTTTGCTAGG GATTAAGCTA TTATGGCTCG GCTACGTTTT CGGCTTACCT 960
375 CTGGCTCTGG GCTTTTCCAT TCCTGAAGTA TTAATTGGTG CTTCGGTAAC CTATATGACC 1020
377 TATGGCATCG TGGTTTGCAC CATCTTTATG CTGGCCCATG TGTGGAATC AACTGAATTT 1080
379 CTCACCCCG ATGGTGAATC CGGTGCCATT GATGACGAGT GGGCTATTTG CCAAATTCGT 1140
381 ACCACGGCCA ATTTTGCCAC CAATAATCCC TTTTGGAAC TTTTGTGG CGGTTTAAAT 1200
383 CACCAAGTTA CCCACCATCT TTTCCCAAT ATTTGTCATA TTCACTATCC CCAATTGGAA 1260
385 AATATTATTA AGGATGTTTG CCAAGAGTTT GGTGTGGAAT ATAAAGTTA TCCCACCTTC 1320
387 AAAGCGGCGA TCGCCTCTAA CTATCGCTGG CTAGAGGCCA TGGGCAAAGC ATCGTGACAT 1380

VERIFICATION SUMMARY

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L:31 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:32 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]